```
Db          3 CTTCGTCTTTGCA 15


RESULT 4
AAF51541
ID   AAF51541 standard; DNA; 15 BP.
XX
AC   AAF51541;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2501.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 77; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 13;  DB 1;  Length 15;
  Best Local Similarity   53.8%;  Pred. No. 1.8;
  Matches    7;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCUUUGCA 13
              |::||:|:::|||
Db          2 CTTCGTCTTTGCA 14


RESULT 5
```



```
AAF51543
ID   AAF51543 standard; DNA; 15 BP.
XX
AC   AAF51543;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2503.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 77; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             92.3%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 2.5;
  Matches    6;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUUUGCA 13
              ::||:|:::|||
Db          1 TTCGTCTTTGCA 12


RESULT 6
AAF51539
ID   AAF51539 standard; DNA; 15 BP.
XX
AC   AAF51539;
```

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: September 1, 2006, 12:04:34 ; Search time 0.001 Seconds
(without alignments)
9.490 Million cell updates/sec

Title: us-09-847-601b-88
Perfect score: 13
Sequence: 1 cuucgucuuugca 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 34 seqs, 365 residues

Total number of hits satisfying chosen parameters: 68

Minimum DB seq length: 5
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 34 summaries

Database : rngdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		13	100.0	13	1	ABZ72849	IGF1 Rz1 ribozyme
2		13	100.0	15	1	AAF51542	IGF-I oligonucleot
3		13	100.0	15	1	AAF51540	IGF-I oligonucleot
4		13	100.0	15	1	AAF51541	IGF-I oligonucleot
5		12	92.3	15	1	AAF51543	IGF-I oligonucleot
6		12	92.3	15	1	AAF51539	IGF-I oligonucleot
7	c	10	76.9	10	1	AAF38544	Yeast NORF gene SA
8		9	69.2	10	1	AAF41570	Yeast NORF gene SA
9		9	69.2	10	1	AAF35016	Yeast NORF gene SA
10		9	69.2	10	1	AAF35467	Yeast NORF gene SA
11	c	9	69.2	10	1	AAF34844	Yeast NORF gene SA
12	c	8.4	64.6	10	1	AAF34839	Yeast NORF gene SA
13		8.4	64.6	10	1	AAF42946	Yeast NORF gene SA
14	c	8.4	64.6	10	1	AAF42256	Yeast NORF gene SA
15	c	8.4	64.6	10	1	AAF36161	Yeast NORF gene SA
16		8.4	64.6	10	1	AAF43800	Yeast NORF gene SA
17	c	8.4	64.6	10	1	AAF38546	Yeast NORF gene SA
18	c	8.4	64.6	10	1	AAF40426	Yeast NORF gene SA
19		8.4	64.6	10	1	ABK96059	Human LIPE gene po
20		8.4	64.6	10	1	ADI13726	Cytoplasmic tumour
21		8.4	64.6	10	1	ADU50908	Analyte detection-
22	c	8	61.5	10	1	AAZ82055	Metastatic breast
23		8	61.5	10	1	AAH63934	Human ubiquitously
24	c	8	61.5	10	1	AAF34140	Yeast NORF gene SA
25		8	61.5	10	1	AAF42583	Yeast NORF gene SA
26	c	8	61.5	10	1	AAF37269	Yeast NORF gene SA
27	c	8	61.5	10	1	AAF38836	Yeast NORF gene SA
28	c	8	61.5	10	1	AAF42254	Yeast NORF gene SA
29	c	8	61.5	10	1	AAF34626	Yeast NORF gene SA
30		8	61.5	10	1	AAF43668	Yeast NORF gene SA
31	c	8	61.5	10	1	AAF40632	Yeast NORF gene SA
32	c	8	61.5	10	1	ACC69588	D. melanogaster 42
33		7.4	56.9	9	1	AAD08670	Human OY-TES-1 ful
34		7	53.8	8	1	ABK29982	Hepatitis B virus

ALIGNMENTS

RESULT 1
ABZ72849
ID ABZ72849 standard; RNA; 13 BP.
XX
AC ABZ72849;
XX
DT 09-APR-2003 (first entry)
XX
DE IGF1 Rz1 ribozyme target sequence SEQ ID NO:88.
XX
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS Synthetic.
XX
PN WO200288320-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-US013679.
XX
PR 01-MAY-2001; 2001US-00847601.
XX
PA (UYFL) UNIV FLORIDA.
XX
PI Lewin AS, Shaw LC, Grant MB;
XX
DR WPI; 2003-111880/10.
XX
PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX
PS Claim 1; Page 80; 115pp; English.
XX
CC The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, iNOS,
CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC dysfunction, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC exemplification of the present invention
XX

```
SQ   Sequence 13 BP; 1 A; 4 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match           100.0%;  Score 13;  DB 1;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 2.1;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCUUUGCA 13
              |||||||||||||
Db          1 CUUCGUCUUUGCA 13


RESULT 2
AAF51542
ID   AAF51542 standard; DNA; 15 BP.
XX
AC   AAF51542;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2502.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 77; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 13;  DB 1;  Length 15;
  Best Local Similarity  53.8%;  Pred. No. 1.8;
  Matches    7;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCUUUGCA 13
              |::||:|:::|||
Db          1 CTTCGTCTTTGCA 13


RESULT 3
AAF51540
ID   AAF51540 standard; DNA; 15 BP.
XX
AC   AAF51540;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2500.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 77; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 13;  DB 1;  Length 15;
  Best Local Similarity  53.8%;  Pred. No. 1.8;
  Matches    7;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCUUUGCA 13
              |::||:|:::|||
```

```
Db          3 CTTCGTCTTTGCA 15


RESULT 4
AAF51541
ID   AAF51541 standard; DNA; 15 BP.
XX
AC   AAF51541;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2501.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 77; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
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CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
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CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 13;  DB 1;  Length 15;
  Best Local Similarity   53.8%;  Pred. No. 1.8;
  Matches    7;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCUUUGCA 13
              |::||:|:::|||
Db          2 CTTCGTCTTTGCA 14


RESULT 5
```

```
AAF51543
ID   AAF51543 standard; DNA; 15 BP.
XX
AC   AAF51543;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2503.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 77; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             92.3%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 2.5;
  Matches    6;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUUUGCA 13
              ::||:|:::|||
Db          1 TTCGTCTTTGCA 12


RESULT 6
AAF51539
ID   AAF51539 standard; DNA; 15 BP.
XX
AC   AAF51539;
```

```
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2499.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 77; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 5 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             92.3%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 2.5;
  Matches    6;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCUUUGC 12
              |::||:|:::||
Db          4 CTTCGTCTTTGC 15


RESULT 7
AAF38544/c
ID   AAF38544 standard; DNA; 10 BP.
XX
AC   AAF38544;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5283.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 188; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             76.9%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 7.7;
  Matches    4;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCUUU 10
              |::||:|:::
Db         10 CTTCGTCTTT 1


RESULT 8
AAF41570
ID   AAF41570 standard; DNA; 10 BP.
XX
AC   AAF41570;
XX
```

DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8309.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 296; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 69.2%; Score 9; DB 1; Length 10;
Best Local Similarity 44.4%; Pred. No. 11;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUUCGUCUU 9
|::||:|::
Db 1 CTTCGTCTT 9

RESULT 9
AAF35016
ID AAF35016 standard; DNA; 10 BP.
XX
AC AAF35016;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1755.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 62; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 69.2%; Score 9; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 11;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2 UUCGUCUUU 10
::||:|:::
Db 1 TTCGTCTTT 9

```
RESULT 10
AAF35467
ID   AAF35467 standard; DNA; 10 BP.
XX
AC   AAF35467;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2206.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 78; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             69.2%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   44.4%;  Pred. No. 11;
  Matches    4;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCUU 9
              |::||:|::
Db          2 CTTCGTCTT 10


RESULT 11
AAF34844/c
ID   AAF34844 standard; DNA; 10 BP.
XX
AC   AAF34844;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1583.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 56; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             69.2%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   44.4%;  Pred. No. 11;
  Matches    4;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 CUUCGUCUU 9
              |::||:|::
Db          9 CTTCGTCTT 1
```

RESULT 12
AAF34839/c
ID AAF34839 standard; DNA; 10 BP.
XX
AC AAF34839;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1578.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 56; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 7 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 64.6%; Score 8.4; DB 1; Length 10;
Best Local Similarity 30.0%; Pred. No. 13;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 CUUCGUCUUU 10
              |::| :|:::
Db         10 CTTCTTCTTT 1
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RESULT 13
AAF42946
ID AAF42946 standard; DNA; 10 BP.
XX
AC AAF42946;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11085.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 345; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

```
XX
SQ   Sequence 10 BP; 0 A; 3 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match             64.6%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 13;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 UCGUCUUUGC 12
              :||:|::: |
Db          1 TCGTCTTTTC 10


RESULT 14
AAF42256/c
ID   AAF42256 standard; DNA; 10 BP.
XX
AC   AAF42256;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8995.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 321; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             64.6%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 13;
  Matches    5;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 UCGUCUUUGC 12
              :|| |:::||
Db         10 TCGCCTTTGC 1


RESULT 15
AAF36161/c
ID   AAF36161 standard; DNA; 10 BP.
XX
AC   AAF36161;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2900.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 103; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
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CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             64.6%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 13;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCUUU 10
              |::||:| ::
Db         10 CTTCGTCGTT 1


RESULT 16
AAF43800
ID   AAF43800 standard; DNA; 10 BP.
XX
AC   AAF43800;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11939.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 376; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 0 A; 1 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             64.6%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   30.0%;  Pred. No. 13;
  Matches    3;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUUUG 11
              :: |:|:::|
Db          1 TTGGTCTTTG 10


RESULT 17
AAF38546/c
ID   AAF38546 standard; DNA; 10 BP.
XX
AC   AAF38546;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5285.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 188; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
```

CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 64.6%; Score 8.4; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CUUCGUCUUU 10
|: ||:|:::
Db 10 CTCCGTCTTT 1

RESULT 18
AAF40426/c
ID AAF40426 standard; DNA; 10 BP.
XX
AC AAF40426;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7165.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 255; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 7 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 64.6%; Score 8.4; DB 1; Length 10;
Best Local Similarity 30.0%; Pred. No. 13;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 2 UUCGUCUUUG 11
::||: :::|
Db 10 TTCGTTTTTG 1

RESULT 19
ABK96059
ID ABK96059 standard; DNA; 10 BP.
XX
AC ABK96059;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human LIPE gene polymorphism detection oligonucleotide primer #34.
XX
KW Human; lipase; hormone sensitive; LIPE; isogene; obesity; male sterility;
KW polymorphism; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200240502-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-US043518.
XX
PR 16-NOV-2000; 2000US-0249302P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Bentivegna SC, Chew A, Koshy B, Rounds E;
XX
DR WPI; 2002-519369/55.
XX
PT Novel genetic variants of Lipase, Hormone-Sensitive isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT diseases associated with LIPE activity, e.g. obesity and male sterility.
XX
PS Claim 17; Page 16; 142pp; English.
XX
CC The present invention relates to a new polynucleotide comprising a
CC nucleotide sequence which comprises lipase, hormone sensitive (LIPE)
CC isogenes. The invention is useful in screening for drugs targeting LIPE
CC isogenes that are useful for treating obesity and male sterility. The
CC methods of the invention are useful for improving the efficiency and
CC reliability of several steps in the discovery and development of drugs
CC for treating diseases associated with LIPE activity. The polynucleotide
CC is useful in studying the expression and function of LIPE, and in
CC expressing LIPE protein for use in screening for candidate drugs to treat
CC diseases related to LIPE activity. It is also useful in studying the
CC effect of the variation on the biological activity of LIPE as well as on

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CC   the binding affinity of candidate drugs targeting LIPE for the treatment
CC   of obesity and male sterility. The invention is useful for studying the
CC   expression of LIPE isogenes in vivo, for in vivo screening and testing of
CC   drugs targeted against LIPE protein, and for testing the efficacy of
CC   therapeutic agents and compounds for treating obesity and male sterility
CC   in a biological system. The present nucleic acid sequence represents one
CC   of a collection (ABK96026-ABK96083) of oligonucleotide primers that were
CC   used in the invention to detect polymorphisms in the human LIPE gene
XX
SQ   Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             64.6%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 13;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUUUG 11
              : ||:|:::|
Db          1 TCCGTCTTTG 10


RESULT 20
ADI13726
ID   ADI13726 standard; DNA; 10 BP.
XX
AC   ADI13726;
XX
DT   22-APR-2004  (first entry)
XX
DE   Cytoplasmic tumour endothelial marker standard tag SEQ ID NO:101.
XX
KW   tumour endothelial marker; TEM; endothelial cell regulation;
KW   neoangiogenesis inhibition; neoangiogenesis screening;
KW   neoangiogenesis promotion; neoangiogenesis; tumour; wound healing;
KW   cytostatic; vulnerary; human; standard tag; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004005883-A2.
XX
PD   15-JAN-2004.
XX
PF   02-JUL-2003; 2003WO-US016250.
XX
PR   02-JUL-2002; 2002US-0393023P.
PR   01-APR-2003; 2003US-0458964P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   St Croix B,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 2004-142995/14.
XX
PT   Use of tumor endothelial marker proteins for inhibiting neoangiogenesis,
PT   screening for neoangiogenesis, promoting neoangiogenesis, identifying
PT   candidate drugs for treating tumors or promoting wound healing.
XX
PS   Disclosure; SEQ ID NO 101; 113pp; English.
XX
CC   The present invention describes the use of tumour endothelial marker
CC   (TEM) proteins for identifying a ligand involved in endothelial cell
CC   regulation, inhibiting neoangiogenesis, screening for neoangiogenesis,
CC   promoting neoangiogenesis, identifying candidate drugs for treating
CC   tumours or promoting wound healing or identifying endothelial cells. Also
CC   described: (1) identification of a ligand involved in endothelial cell
CC   regulation; (2) inhibiting neoangiogenesis; (3) promoting neoangiogenesis
CC   in a patient; (4) screening for neoangiogenesis in a patient; (5)
CC   identify candidate drugs for treating tumours or promoting wound healing;
CC   and (6) identifying endothelial cells. TEM proteins have cytostatic and
CC   vulnerary activities. The TEM proteins are useful for identifying a
CC   ligand involved in endothelial cell regulation, inhibiting
CC   neoangiogenesis, screening for neoangiogenesis, promoting
CC   neoangiogenesis, identifying candidate drugs for treating tumours or
CC   promoting wound healing or identifying endothelial cells. The present
CC   sequence represents a cytoplasmic tumour endothelial marker standard tag
CC   oligonucleotide, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             64.6%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 13;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 UCGUCUUUGC 12
              :| :|:::||
Db          1 TCATCTTTGC 10


RESULT 21
ADU50908
ID   ADU50908 standard; DNA; 10 BP.
XX
AC   ADU50908;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Analyte detection-related human p53-targeting oligonucleotide probe #8.
XX
KW   analyte detection; probe; ss; p53.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004097371-A2.
XX
PD   11-NOV-2004.
XX
PF   26-APR-2004; 2004WO-US012916.
XX
PR   25-APR-2003; 2003US-0465336P.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Schmid MJ,  Willson GC;
XX
DR   WPI; 2005-012657/01.
XX
PT   Analyte detection device, has sensing elements coupled with probes that
PT   are capable of producing signal when analyte interacts with probe and
PT   determining identity of analyte based on signal produced by sensing
PT   element.
XX
PS   Example; Fig 2; 32pp; English.
XX
CC   This invention relates to a novel analyte detection device, having
CC   several sensing elements, where one or more probes are coupled to each of
CC   the sensing elements, and where at least one of the probes is configured
CC   to interact with an analyte, and where at least one sensing element
CC   produces a signal when the analyte interacts with a probe, and where
CC   sensing elements produce detectable signals in predetermined pattern that
CC   represents a code that identifies analyte. The invention is useful for
CC   analyzing analytes such as DNA, RNA, proteins, enzymes, oligopeptides,
CC   antigens, antibodies or organic molecules. The present sequence is that
CC   of an oligonucleotide probe which targets a region of the human p53 gene
CC   and which was used in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             64.6%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 13;
  Matches    4;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUUUG 11
              : ||:|:::|
Db          1 TGCGTCTTTG 10
```

```
RESULT 22
AAZ82055/c
ID   AAZ82055 standard; DNA; 10 BP.
XX
AC   AAZ82055;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1289.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 93; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             61.5%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   37.5%;  Pred. No. 15;
  Matches    3;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUU 9
              ::||:|::
Db          9 TTCGTCTT 2


RESULT 23
AAH63934
ID   AAH63934 standard; cDNA; 10 BP.
XX
AC   AAH63934;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 774.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 13; Page 56; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match             61.5%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   37.5%;  Pred. No. 15;
  Matches    3;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 UCGUCUUU 10
              :||:|:::
Db          1 TCGTCTTT 8


RESULT 24
AAF34140/c
ID   AAF34140 standard; DNA; 10 BP.
XX
AC   AAF34140;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:879.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
```

```
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 31; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             61.5%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 15;
  Matches    4;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GUCUUUGC 12
              |:|:::||
Db          8 GTCTTTGC 1


RESULT 25
AAF42583
ID   AAF42583 standard; DNA; 10 BP.
XX
AC   AAF42583;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10722.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 332; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             61.5%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 15;
  Matches    4;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 UCUUUGCA 13
              :|:::|||
Db          3 TCTTTGCA 10


RESULT 26
AAF37269/c
ID   AAF37269 standard; DNA; 10 BP.
XX
AC   AAF37269;
XX
DT   23-MAR-2001  (first entry)
XX
```

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4008.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 143; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 6 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 UCUUUGCA 13
:|:::|||
Db 9 TCTTTGCA 2

RESULT 27
AAF38836/c
ID AAF38836 standard; DNA; 10 BP.
XX
AC AAF38836;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5575.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 199; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 15;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 2 UUCGUCUU 9
::||:|::
Db 8 TTCGTCTT 1

RESULT 28
AAF42254/c

ID AAF42254 standard; DNA; 10 BP.
XX
AC AAF42254;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8993.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 321; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GUCUUUGC 12
|:|:::||
Db 8 GTCTTTGC 1

RESULT 29
AAF34626/c
ID AAF34626 standard; DNA; 10 BP.
XX
AC AAF34626;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1365.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 48; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 15;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 3 UCGUCUUU 10

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              :||:|:::
Db          10 TCGTCTTT 3


RESULT 30
AAF43668
ID   AAF43668 standard; DNA; 10 BP.
XX
AC   AAF43668;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11807.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 371; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             61.5%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 15;
  Matches    4;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 UCUUUGCA 13
              :|:::|||
Db          2 TCTTTGCA 9


RESULT 31
AAF40632/c
ID   AAF40632 standard; DNA; 10 BP.
XX
AC   AAF40632;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7371.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 263; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
```

```
  Query Match             61.5%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 15;
  Matches    4;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCU 8
              |::||:|:
Db          9 CTTCGTCT 2


RESULT 32
ACC69588/c
ID   ACC69588 standard; DNA; 10 BP.
XX
AC   ACC69588;
XX
DT   16-JUL-2003  (first entry)
XX
DE   D. melanogaster 42 bp deletion flanking oligonucleotide SEQ ID NO:20.
XX
KW   Drosophila; insecticide; cyp6g1; pesticide; ss.
XX
OS   Drosophila melanogaster.
OS   Synthetic.
XX
PN   WO2003025223-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-GB004213.
XX
PR   20-SEP-2001; 2001GB-00022693.
XX
PA   (UYBA-) UNIV BATH.
XX
PI   Ffrench-Constant RH,  Daborn PJ;
XX
DR   WPI; 2003-333171/31.
XX
PT   Use of a cell, cell line or organism in which the activity of Drosophila
PT   melanogaster gene cyp6g1, is increased relative to wild type activity of
PT   cyp6g1, for the screening of putative pesticides.
XX
PS   Claim 12; Page 59; 85pp; English.
XX
CC   The present invention describes the use of a cell, cell line or organism
CC   (collectively referred to as (I)) in which the activity of the Drosophila
CC   melanogaster gene cyp6g1, its derivatives or fragments, is increased
CC   relative to wild type activity of cyp6g1, for the screening of putative
CC   pesticides. Also described: (1) testing a putative pesticide for its
CC   potential resistance, by contacting (I) and detecting any detrimental
CC   effect on (I); (2) testing a putative pesticide for its potential
CC   resistance, by contacting (I) comprising a transposable element and
CC   detecting any detrimental effect on (I); and (3) a pesticide whose
CC   activity is detected by the above method; (I) is useful in the screening
CC   of putative pesticides. The present sequence represents an
CC   oligonucleotide which flanks a 42 bp deletion of Drosophila melanogaster
CC   cyp6g1, which is used in an example from the present invention
XX
SQ   Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             61.5%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   37.5%;  Pred. No. 15;
  Matches    3;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUU 9
              ::||:|::
Db         10 TTCGTCTT 3


RESULT 33
AAD08670
ID   AAD08670 standard; DNA; 9 BP.
XX
AC   AAD08670;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human OY-TES-1 full length cDNA isolating 5' RACE-PCR primer #2.
XX
KW   Human; cytostatic; fibrosarcoma cancer; cancer associated antigen; RACE;
KW   rapid amplification of cDNA end; gene therapy; vaccine; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200140271-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US032750.
XX
PR   01-DEC-1999;   99US-0168353P.
PR   26-APR-2000; 2000US-00559013.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Ono T,  Nakayama E;
XX
DR   WPI; 2001-397941/42.
XX
PT   Isolated polypeptide, useful in treating disorders such as cancer, is
PT   encoded by a nucleic acid (NA) Group 3 or 4 molecule.
XX
PS   Example 2; Page 70; 127pp; English.
XX
CC   The invention relates to cancer associated antigens and their nucleic
CC   acids which are expressed in methylcholanthrene-induced fibrosarcoma
CC   cancer cells from mice. Cancer associated antigens and a pharmaceutical
CC   composition containing nucleic acid molecules encoding cancer associated
CC   antigens are used to treat a condition e.g. cancer. Cancer associated
CC   antigens, the nucleotides encoding them, antibodies against them and the
CC   pharmaceutical compositions comprising them are useful for diagnosing,
CC   monitoring and treating the diseases characterised by the expression of
CC   one or more cancer associated antigens, e.g. fibrosarcoma cancer, and for
CC   research purposes. Cancer associated antigens DNA is also useful in gene
CC   therapy. The present sequence is 5'RACE (rapid amplification of cDNA end)
CC   PCR primer used for isolating human full length OY-TES-1 cDNA
XX
SQ   Sequence 9 BP; 0 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             56.9%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 77;
  Matches    3;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCUU 9
              |::||: ::
Db          1 CTTCGTGTT 9


RESULT 34
ABK29982
ID   ABK29982 standard; DNA; 8 BP.
XX
AC   ABK29982;
XX
DT   23-APR-2002  (first entry)
XX
DE   Hepatitis B virus (HBV) domain 12-1 wild type.
XX
KW   Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
KW   HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
KW   vanH promoter; androgen receptor promoter; AR promoter;
KW   human epidermal growth factor receptor 2 promoter; her2 promoter;
KW   beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
KW   colon cancer; immunological disorder; prostate cancer; cytostatic;
KW   autoimmune disease; HBV pre-S promoter; HBV-X promoter;
```

KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;
KW gene expression modulator; multiple sclerosis; MS;
KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
KW transgenic; ds.
XX
OS Hepatitis B virus.
XX
PN WO200194600-A2.
XX
PD 13-DEC-2001.
XX
PF 06-JUN-2001; 2001WO-US018343.
XX
PR 06-JUN-2000; 2000US-0209549P.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;
PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;
PI Lim MY, Bruice TW;
XX
DR WPI; 2002-130595/17.
XX
PT New nucleic acid regulatory sequences, which are able to regulate
PT expression of a gene operably linked to a promoter, useful for regulating
PT the expression of transgenes and for treating e.g., cancer and
PT immunological diseases.
XX
PS Example 3; Page 43; 95pp; English.
XX
CC The invention describes an isolated nucleic acid regulatory sequence for
CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
CC (Bla) promoter. Transcription regulatory sequences may be used to
CC regulate expression of the endogenous, autologous or heterologous genes
CC operably linked to the promoter, and may be incorporated into
CC heterologous nucleic acid constructs for use in regulated expression of
CC transgenes. Regulated expression of cyclin D1 can be used in cancer
CC therapies, such as breast, colon or pancreatic cancers and familial
CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
CC may be used in the treatment of immunological disorders, such as
CC autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus
CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
CC arthritis. Regulated expression of genes under the control of the HBV
CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
CC hepatocellular carcinoma, and in the regulated expression of liver cell-
CC specific genes. Regulated expression of the vanH gene promoter can be
CC used in treatment of Enterococcus infection, while regulated expression
CC of the androgen receptor gene can be used in the treatment of prostate
CC cancer. This represents the wild type sequence of a promoter region used
CC in the invention to create mutant promoter fragments to determine the
CC regulatory regions involved in gene expression, described in the method
CC of the invention
XX
SQ Sequence 8 BP; 0 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 53.8%; Score 7; DB 1; Length 8;
Best Local Similarity 42.9%; Pred. No. 87;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 GUCUUUG 11
              |:|:::|
Db          1 GTCTTTG 7
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Search completed: September 1, 2006, 12:04:34
Job time : 0.001 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: September 1, 2006, 12:03:21 ; Search time 0.001 Seconds
(without alignments)
3.848 Million cell updates/sec

Title: us-09-847-601b-88
Perfect score: 13
Sequence: 1 cuucgucuuugca 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 17 seqs, 148 residues

Total number of hits satisfying chosen parameters: 34

Minimum DB seq length: 5
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 17 summaries

Database : rgedb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13	100.0	13	1	AR407995	ACCESSION:AR407995
	2	8	61.5	10	1	AR303335	ACCESSION:AR303335
	3	8	61.5	10	1	AX152859	ACCESSION:AX152859
	4	8	61.5	10	1	AX301317	ACCESSION:AX301317
c	5	8	61.5	10	1	AX806339	ACCESSION:AX806339
	6	7.4	56.9	9	1	CS071888	ACCESSION:CS071888
c	7	7.4	56.9	9	1	CS133987	ACCESSION:CS133987
c	8	7	53.8	7	1	CQ766095	ACCESSION:CQ766095
c	9	7	53.8	7	1	CQ766096	ACCESSION:CQ766096
c	10	7	53.8	7	1	CQ766097	ACCESSION:CQ766097
	11	6.4	49.2	8	1	CQ924619	ACCESSION:CQ924619
c	12	6.4	49.2	8	1	E02034	ACCESSION:E02034
	13	6.4	49.2	8	1	AX003298	ACCESSION:AX003298
	14	6.4	49.2	8	1	AX104953	ACCESSION:AX104953
	15	6.4	49.2	8	1	AX211691	ACCESSION:AX211691
	16	6.4	49.2	8	1	AX358376	ACCESSION:AX358376
c	17	6.4	49.2	8	1	AX358378	ACCESSION:AX358378

ALIGNMENTS

RESULT 1
AR407995
LOCUS AR407995 13 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 88 from patent US 6632057.
ACCESSION AR407995
VERSION AR407995.1 GI:40157982
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 88 14-OCT-2003;
GFI Aerospace; Paris;
FRX;
FEATURES Location/Qualifiers
source 1. .13
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 100.0%; Score 13; DB 1; Length 13;
Best Local Similarity 53.8%; Pred. No. 0.28;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CUUCGUCUUUGCA 13
|::||:|:::|||
Db 1 CTTCGTCTTTGCA 13

RESULT 2
AR303335
LOCUS AR303335 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 60 from patent US 6544736.
ACCESSION AR303335
VERSION AR303335.1 GI:31692111
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 60 08-APR-2003;
Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo;
JPX;
FEATURES Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GUCUUUGC 12
|:|:::||
Db 2 GTCTTTGC 9

RESULT 3
AX152859
LOCUS AX152859 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 774 from Patent WO0138577.
ACCESSION AX152859
VERSION AX152859.1 GI:14534510
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 774 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

```
  Query Match            61.5%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  37.5%;  Pred. No. 2;
  Matches    3;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 UCGUCUUU 10
              :||:|:::
Db          1 TCGTCTTT 8


RESULT 4
AX301317
LOCUS       AX301317                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 31 from Patent WO0185941.
ACCESSION   AX301317
VERSION     AX301317.1  GI:17382400
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 31 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            61.5%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  37.5%;  Pred. No. 2;
  Matches    3;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 UCGUCUUU 10
              :||:|:::
Db          1 TCGTCTTT 8


RESULT 5
AX806339/c
LOCUS       AX806339                  10 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 20 from Patent WO03025223.
ACCESSION   AX806339
VERSION     AX806339.1  GI:38523027
KEYWORDS    .
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1
  AUTHORS   French-Constant,R.H. and Daborn,P.J.
  TITLE     Improvements in or relating to insecticide screening
  JOURNAL   Patent: WO 03025223-A 20 27-MAR-2003;
            UNIVERSITY OF BATH (GB)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Drosophila melanogaster"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:7227"
                     /note="Sequence flanking 42 bp deletion in 5#UTR"

  Query Match            61.5%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  37.5%;  Pred. No. 2;
  Matches    3;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUU 9
              ::||:|::
Db         10 TTCGTCTT 3


RESULT 6
CS071888
LOCUS       CS071888                   9 bp    DNA     linear   PAT 05-MAY-2005
DEFINITION  Sequence 36 from Patent WO2001040271.
ACCESSION   CS071888
VERSION     CS071888.1  GI:63089211
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ono,T. and Nakayama,E.
  TITLE     Cancer associated antigens and uses therefor
  JOURNAL   Patent: WO 2001040271-A 36 07-JUN-2001;
            Ludwig Institute for Cancer Research (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            56.9%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity  33.3%;  Pred. No. 12;
  Matches    3;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCUU 9
              |::||: ::
Db          1 CTTCGTGTT 9


RESULT 7
CS133987/c
LOCUS       CS133987                   9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 529 from Patent WO2005058479.
ACCESSION   CS133987
VERSION     CS133987.1  GI:71793536
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 529 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match            56.9%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity  44.4%;  Pred. No. 12;
  Matches    4;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 UCGUCUUUG 11
              :||:| ::|
Db          9 TCGTCGTTG 1


RESULT 8
CQ766095/c
LOCUS       CQ766095                   7 bp    DNA     linear   PAT 03-MAR-2004
DEFINITION  Sequence 56 from Patent WO2004005547.
ACCESSION   CQ766095
VERSION     CQ766095.1  GI:44908355
KEYWORDS    .
SOURCE      synthetic construct
```

```
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Weinzierl,R.
  TITLE     Method
  JOURNAL   Patent: WO 2004005547-A 56 15-JAN-2004;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HS consensus sequence"

  Query Match             53.8%;  Score 7;  DB 1;  Length 7;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    3;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CGUCUUU 10
              ||:|:::
Db          7 CGTCTTT 1


RESULT 9
CQ766096/c
LOCUS       CQ766096                  7 bp    DNA     linear   PAT 03-MAR-2004
DEFINITION  Sequence 57 from Patent WO2004005547.
ACCESSION   CQ766096
VERSION     CQ766096.1  GI:44908356
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Weinzierl,R.
  TITLE     Method
  JOURNAL   Patent: WO 2004005547-A 57 15-JAN-2004;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HS consensus sequence"

  Query Match             53.8%;  Score 7;  DB 1;  Length 7;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    3;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CGUCUUU 10
              ||:|:::
Db          7 CGTCTTT 1


RESULT 10
CQ766097/c
LOCUS       CQ766097                  7 bp    DNA     linear   PAT 03-MAR-2004
DEFINITION  Sequence 58 from Patent WO2004005547.
ACCESSION   CQ766097
VERSION     CQ766097.1  GI:44908357
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Weinzierl,R.
  TITLE     Method
  JOURNAL   Patent: WO 2004005547-A 58 15-JAN-2004;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HS consensus sequence"

  Query Match             53.8%;  Score 7;  DB 1;  Length 7;
  Best Local Similarity   42.9%;  Pred. No. 15;
  Matches    3;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CGUCUUU 10
              ||:|:::
Db          7 CGTCTTT 1


RESULT 11
CQ924619
LOCUS       CQ924619                  8 bp    DNA     linear   PAT 23-NOV-2004
DEFINITION  Sequence 3 from Patent WO2004097043.
ACCESSION   CQ924619
VERSION     CQ924619.1  GI:56214216
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Douglas,K.T., Bichenkova,E.V., Savage,H. and Sardarian,A.U.
  TITLE     Exciplexes
  JOURNAL   Patent: WO 2004097043-A 3 11-NOV-2004;
            THE VICTORIA UNIVERSITY OF MANCHESTER (GB)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="8mer labelled probe"

  Query Match             49.2%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 13;
  Matches    4;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GUCUUUGC 12
              |:|:: ||
Db          1 GTCTTAGC 8


RESULT 12
E02034/c
LOCUS       E02034                    8 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA sequence before initiation codon containing initiation codon.
ACCESSION   E02034
VERSION     E02034.1  GI:22026665
KEYWORDS    JP 1989196296-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Sakurai,T., Naruto,M. and Ozawa,H.
  TITLE     MANIFESTATION VECTOR FOR ANIMAL CELL
  JOURNAL   Patent: JP 1989196296-A 1 08-AUG-1989;
            TORAY IND INC
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1989196296-A/1
            PD   08-AUG-1989
            PF   29-JAN-1988 JP 1988020174
            PI   SAKURAI TORU, NARUTO MASANOBU, OZAWA HITOSHI
            PC   C12N15/00;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   CDS             6. .>8
            FT                   /Codon_start=1.
```

```
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             49.2%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   37.5%;  Pred. No. 13;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CGUCUUUG 11
              | :|:::|
Db          8 CATCTTTG 1


RESULT 13
AX003298
LOCUS       AX003298                  8 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 33 from Patent WO9929871.
ACCESSION   AX003298
VERSION     AX003298.1  GI:9927115
KEYWORDS    .
SOURCE      Circovirus
  ORGANISM  Circovirus
            Viruses; ssDNA viruses; Circoviridae.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Hutet,E., Albina,E., Arnauld,C., Cariolet,R., Jestin,A., Le,C.P.,
            Madec,F., Mahe,D., Blanchard,P. and Truong,C.
  TITLE     Circovirus sequences related to piglet weight loss disease (pwd)
  JOURNAL   Patent: WO 9929871-A 33 17-JUN-1999;
            HUTET EVELYNE (FR); ALBINA EMMANUEL (FR); ARNAULD CLAIRE (FR);
            CARIOLET ROLAND (FR); JESTIN ANDRE (FR); LE CANN PIERRE (FR); MADEC
            FRANCOIS (FR); MAHE DOMINIQUE (FR); BLANCHARD PHILIPPE (FR); TRUONG
            CATHERINE (FR); VETERINAIRES ET ALIMENTAIRES C (FR)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="Circovirus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:39725"

  Query Match             49.2%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   37.5%;  Pred. No. 13;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUU 9
              : ||:|::
Db          1 TCCGTCTT 8


RESULT 14
AX104953
LOCUS       AX104953                  8 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 1145 from Patent WO0122972.
ACCESSION   AX104953
VERSION     AX104953.1  GI:13921150
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 1145 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             49.2%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   37.5%;  Pred. No. 13;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 UCGUCUUU 10
              :||:| ::
Db          1 TCGTCGTT 8


RESULT 15
AX211691
LOCUS       AX211691                  8 bp    mRNA    linear   PAT 06-SEP-2001
DEFINITION  Sequence 21 from Patent WO0159138.
ACCESSION   AX211691
VERSION     AX211691.1  GI:15523923
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Vanderhaeghen,R. and van Lijsebettens,M.
  TITLE     Plant internal ribosome entry segment
  JOURNAL   Patent: WO 0159138-A 21 16-AUG-2001;
            Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="effector sequence"

  Query Match             49.2%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   37.5%;  Pred. No. 13;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CUUCGUCU 8
              |::| :|:
Db          1 CTTCTTCT 8


RESULT 16
AX358376
LOCUS       AX358376                  8 bp    mRNA    linear   PAT 13-FEB-2002
DEFINITION  Sequence 3 from Patent WO0191536.
ACCESSION   AX358376
VERSION     AX358376.1  GI:18675012
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Wang,D.
  TITLE     Genetic vaccine that mimics natural viral infection and induces
            long-lasting immunity to pathogens
  JOURNAL   Patent: WO 0191536-A 3 06-DEC-2001;
            Genphar, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="modified RNA editing site"

  Query Match             49.2%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   25.0%;  Pred. No. 13;
  Matches    2;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUU 9
              ::| :|::
Db          1 TTCTTCTT 8


RESULT 17
AX358378/c
LOCUS       AX358378                  8 bp    DNA     linear   PAT 13-FEB-2002
```

```
DEFINITION  Sequence 5 from Patent WO0191536.
ACCESSION   AX358378
VERSION     AX358378.1  GI:18675014
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Wang,D.
  TITLE     Genetic vaccine that mimics natural viral infection and induces
            long-lasting immunity to pathogens
  JOURNAL   Patent: WO 0191536-A 5 06-DEC-2001;
            Genphar, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="DNA of modified RNA editing site."

  Query Match             49.2%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   25.0%;  Pred. No. 13;
  Matches    2;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUU 9
              ::| :|::
Db          8 TTCTTCTT 1


Search completed: September  1, 2006, 12:03:21
Job time : 0.001 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: September 1, 2006, 12:06:55 ; Search time 0.001 Seconds
(without alignments)
1.118 Million cell updates/sec

Title: us-09-847-601b-88
Perfect score: 13
Sequence: 1 cuucgucuuugca 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 43 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 5
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 4 summaries

Database : rnpbmdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	100.0	13	1	US-09-847-601B-88	Sequence 88, Appl
2	8.4	64.6	10	1	US-10-832-469-12	Sequence 12, Appl
3	8	61.5	10	1	US-10-330-627-774	Sequence 774, App
4	8	61.5	10	1	US-10-293-222-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-847-601B-88
; Sequence 88, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-88

Query Match 100.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CUUCGUCUUUGCA 13
              |||||||||||||
Db          1 CUUCGUCUUUGCA 13
```

RESULT 2
US-10-832-469-12
; Sequence 12, Application US/10832469
; Publication No. US20050064452A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas Systems
; APPLICANT: Schmid, Matthew J
; APPLICANT: Wilson, C Grant
; TITLE OF INVENTION: SYSTEM AND METHOD FOR THE DETECTION OF ANALYTES
; FILE REFERENCE: 5119-12901
; CURRENT APPLICATION NUMBER: US/10/832,469
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 60/465,336
; PRIOR FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-832-469-12

Query Match 64.6%; Score 8.4; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.5;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 UUCGUCUUUG 11
              : ||:|:::|
Db          1 TGCGTCTTTG 10
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RESULT 3
US-10-330-627-774
; Sequence 774, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-774

Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.7;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 UCGUCUUU 10
              :||:|:::
```

```
Db          1 TCGTCTTT 8


RESULT 4
US-10-293-222-31
; Sequence 31, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
;  APPLICANT: Versteeg, Rogier
;  APPLICANT:  Caron, Hubertus N.
;  TITLE OF INVENTION: MYC targets
;  FILE REFERENCE: 2183-5580US
;  CURRENT APPLICATION NUMBER: US/10/293,222
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: PCT/NL01/00361
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: EP 00201698.8
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: EP 00202284.6
;  PRIOR FILING DATE: 2000-06-29
;  NUMBER OF SEQ ID NOS: 455
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-293-222-31

  Query Match             61.5%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   37.5%;  Pred. No. 1.7;
  Matches    3;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 UCGUCUUU 10
              :||:|:::
Db          1 TCGTCTTT 8


Search completed: September  1, 2006, 12:06:55
Job time : 0.001 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: September 1, 2006, 12:07:57 ; Search time 0.001 Seconds
(without alignments)
1.222 Million cell updates/sec

Title: us-09-847-601b-88
Perfect score: 13
Sequence: 1 cuucgucuuugca 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 9 seqs, 47 residues

Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 5
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 9 summaries

Database : rstdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	5	38.5	5	1	CF332399	ACCESSION:CF332399
c	2	5	38.5	6	1	CA850767	ACCESSION:CA850767
	3	5	38.5	6	1	DU784614	ACCESSION:DU784614
c	4	4	30.8	5	1	CL658581	ACCESSION:CL658581
	5	4	30.8	5	1	CL667999	ACCESSION:CL667999
	6	4	30.8	5	1	CL685291	ACCESSION:CL685291
c	7	4	30.8	5	1	DU643362	ACCESSION:DU643362
c	8	4	30.8	5	1	DU643819	ACCESSION:DU643819
	9	4	30.8	5	1	DX081067	ACCESSION:DX081067

ALIGNMENTS

RESULT 1
CF332399/c
LOCUS CF332399 5 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--08-O07.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-O07, mRNA sequence.
ACCESSION CF332399
VERSION CF332399.1 GI:33813018
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 5)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, .Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .5
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--08-O07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 38.5%; Score 5; DB 1; Length 5;
Best Local Similarity 20.0%; Pred. No. 0;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 UCUUU 10
              :|:::
Db          5 TCTTT 1
```

RESULT 2
CA850767/c
LOCUS CA850767 6 bp mRNA linear EST 01-AUG-2003
DEFINITION D06C11_C11_05.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D06C11 5', mRNA sequence.
ACCESSION CA850767
VERSION CA850767.1 GI:33387560
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 6)
AUTHORS Alkharouf,N., Khan,R. and Matthews,B.
TITLE Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
JOURNAL Genome 47 (2), 380-388 (2004)
PUBMED 15060591
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
FEATURES Location/Qualifiers
source 1. .6
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D06C11"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

Query Match 38.5%; Score 5; DB 1; Length 6;

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  Best Local Similarity   50.0%;  Pred. No. 0;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUC 7
              ::|| |
Db          6 TTCGNC 1


RESULT 3
DU784614
LOCUS       DU784614                  6 bp    DNA     linear   GSS 27-JAN-2006
DEFINITION  HF500_42_54TR HF500_10-06-02 uncultured marine microorganism
            HF500_10-06-02 genomic clone HF500_42_54TR, genomic survey
            sequence.
ACCESSION   DU784614
VERSION     DU784614.1  GI:85798909
KEYWORDS    GSS.
SOURCE      uncultured marine microorganism HF500_10-06-02
  ORGANISM  uncultured marine microorganism HF500_10-06-02
            unclassified sequences; environmental samples.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,
            Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.
            and Karl,D.M.
  TITLE     Comparative genomics reveals ecological trends in stratified
            microbial communities in the ocean's interior
  JOURNAL   Science (2006) In press
COMMENT     Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,
            Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson
            and Edward DeLong
            US DOE Joint Genome Institute
            US DOE Joint Genome Institute
            2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
            Tel: 617-253-5271
            Fax: 617-253-2679
            Email: PMRichardson@lbl.gov; delong@mit.edu
            North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
            DNA library prepared from marine picoplankton in the less than 1.6
            um, greater than 0.22 um fraction. Sample Date: 10/6/2002
            Coordinates: 22.45 N, 158 W Depth 500 m Temperature: 7.25 C
            Salinity: 34.07 psu Oxygen: 118.0 umol/kg
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="uncultured marine microorganism HF500_10-06-02"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:361149"
                     /clone="HF500_42_54TR"
                     /cell_type="marine picoplankton, less than 1.8 um, greater
                     than 0.22 um fraction"
                     /clone_lib="HF500_10-06-02"
                     /note="Vector: pCC1FOS; North Pacific Subtropical Gyre
                     (Hawaii) picoplankton genomic fosmid DNA library prepared
                     from marine picoplankton in the less than 1.6 um, greater
                     than 0.22 um fraction.  Picoplankton collected  at 500 m
                     depth on 10/6/2002, Coordinates: 22.45 N,158 W. Sample
                     Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 500 m
                     Temperature: 7.25 C Salinity: 34.07 psu Oxygen: 118.0
                     umol/kg"

  Query Match           38.5%;  Score 5;  DB 1;  Length 6;
  Best Local Similarity   60.0%;  Pred. No. 0;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CGUCU 8
              ||:|:
Db          1 CGTCT 5


RESULT 4
CL658581/c
LOCUS       CL658581                  5 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0131d_E08 - PRI0131d.B21 (5) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL658581
VERSION     CL658581.1  GI:50141602
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
   PUBMED   14681447
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"

  Query Match           30.8%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 0;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CUUC 4
              |::|
Db          4 CTTC 1


RESULT 5
CL667999
LOCUS       CL667999                  5 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0156c_D12 - PRI0156c.B21 (5) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL667999
VERSION     CL667999.1  GI:50162794
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
   PUBMED   14681447
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
```

```
            Seq primer: T7
            Class: fosmid ends.
FEATURES              Location/Qualifiers
     source           1. .5
                      /organism="Pristionchus pacificus"
                      /mol_type="genomic DNA"
                      /strain="California"
                      /db_xref="taxon:54126"
                      /clone_lib="Mixed stage fosmid library of P. pacificus
                      var. California"
                      /note="Vector: pEpifos-5 Fosmid vector"

  Query Match             30.8%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   25.0%;  Pred. No. 0;
  Matches    1;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 UUUG 11
              :::|
Db          2 TTTG 5


RESULT 6
CL685291
LOCUS       CL685291                  5 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0140d_C11_2 - PRI0140d.BR (5) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL685291
VERSION     CL685291.1  GI:50193442
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
   PUBMED   14681447
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES              Location/Qualifiers
     source           1. .5
                      /organism="Pristionchus pacificus"
                      /mol_type="genomic DNA"
                      /strain="California"
                      /db_xref="taxon:54126"
                      /clone_lib="Mixed stage fosmid library of P. pacificus
                      var. California"
                      /note="Vector: pEpifos-5 Fosmid vector"

  Query Match             30.8%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 0;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UUCG 5
              ::||
Db          1 TTCG 4


RESULT 7
DU643362/c
LOCUS       DU643362                  5 bp    DNA     linear   GSS 27-OCT-2005
DEFINITION  Ciuffi-HIV-293T-wt-2-II1C2.M13R Human Integration Site
            Library-Ciuffi-HIV-293t-wt Homo sapiens genomic, genomic survey
            sequence.
ACCESSION   DU643362
VERSION     DU643362.1  GI:78205732
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Ciuffi,A., Llano,M., Poeschla,E., Hoffmann,C., Leipzig,J.,
            Shinn,P., Ecker,J.R. and Bushman,F.D.
  TITLE     A role for LEDGF/p75 in targeting HIV DNA integration
  JOURNAL   Nat. Med. (2005) In press
COMMENT     Contact: Bushman FD
            Department of Microbiology
            University of Pennsylvania School of Medicine
            402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA
            19104-6076, USA
            Tel: 215 573 8732
            Fax: 215 573 4856
            Email: bushman@mail.med.upenn.edu
            The hg17 (May 2004) freeze of the human genome was used.
            Class: shotgun.
FEATURES              Location/Qualifiers
     source           1. .5
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
                      /cell_type="293T"
                      /clone_lib="Human Integration Site
                      Library-Ciuffi-HIV-293t-wt"
                      /note="Sequences cloned using TOPO vectors."

  Query Match             30.8%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 0;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GUCU 8
              |:|:
Db          5 GTCT 2


RESULT 8
DU643819/c
LOCUS       DU643819                  5 bp    DNA     linear   GSS 27-OCT-2005
DEFINITION  Ciuffi-HIV-293T-wt-2-II1C2.M13F Human Integration Site
            Library-Ciuffi-HIV-293t-wt Homo sapiens genomic, genomic survey
            sequence.
ACCESSION   DU643819
VERSION     DU643819.1  GI:78206189
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Ciuffi,A., Llano,M., Poeschla,E., Hoffmann,C., Leipzig,J.,
            Shinn,P., Ecker,J.R. and Bushman,F.D.
  TITLE     A role for LEDGF/p75 in targeting HIV DNA integration
  JOURNAL   Nat. Med. (2005) In press
COMMENT     Contact: Bushman FD
            Department of Microbiology
            University of Pennsylvania School of Medicine
            402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA
            19104-6076, USA
            Tel: 215 573 8732
            Fax: 215 573 4856
            Email: bushman@mail.med.upenn.edu
            The hg17 (May 2004) freeze of the human genome was used.
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          Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /cell_type="293T"
                     /clone_lib="Human Integration Site
                     Library-Ciuffi-HIV-293t-wt"
                     /note="Sequences cloned using TOPO vectors."

  Query Match             30.8%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 0;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GUCU 8
              |:|:
Db          5 GTCT 2


RESULT 9
DX081067
LOCUS       DX081067                  5 bp    DNA     linear   GSS 10-JAN-2006
DEFINITION  KBrB093N19R KBrB, Brassica rapa BamHI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBrB093N19, genomic survey
            sequence.
ACCESSION   DX081067
VERSION     DX081067.1  GI:84775363
KEYWORDS    GSS.
SOURCE      Brassica rapa subsp. pekinensis
  ORGANISM  Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 5)
  AUTHORS   Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J.H. and Park,B.S.
  TITLE     End sequence of Brassica rapa BamHI (KBrB) BAC clone
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@rda.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
            KBrB093N19
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .5
                     /organism="Brassica rapa subsp. pekinensis"
                     /mol_type="genomic DNA"
                     /cultivar="Chiifu"
                     /sub_species="pekinensis"
                     /db_xref="taxon:51351"
                     /clone="KBrB093N19"
                     /lab_host="E.coli DH10B"
                     /clone_lib="KBrB, Brassica rapa BamHI BAC library"
                     /note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
                     pekinensis var. Chiifu BAC library (KBrB BAC) is provided
                     by Yong-Pyo Lim (CNU)."

  Query Match             30.8%;  Score 4;  DB 1;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 0;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UUCG 5
              ::||
Db          2 TTCG 5
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Job time : 0.001 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: September 1, 2006, 12:05:44 ; Search time 0.001 Seconds
(without alignments)
1.820 Million cell updates/sec

Title: us-09-847-601b-88
Perfect score: 13
Sequence: 1 cuucgucuuugca 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 70 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 5
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 8 summaries

Database : rnidb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	100.0	13	1	US-09-874-601-88	Sequence 88, Appl
2	8	61.5	10	1	US-09-508-753B-60	Sequence 60, Appl
3	6.4	49.2	8	1	US-09-585-599A-3	Sequence 3, Appli
c 4	6.4	49.2	8	1	US-09-585-599A-5	Sequence 5, Appli
5	6.4	49.2	8	1	US-09-514-245-45	Sequence 45, Appl
6	6.4	49.2	8	1	US-10-327-294-3	Sequence 3, Appli
c 7	6.4	49.2	8	1	US-10-327-294-5	Sequence 5, Appli
c 8	6	46.2	7	1	US-09-432-020B-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-874-601-88
; Sequence 88, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-88

Query Match 100.0%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CUUCGUCUUUGCA 13
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Db          1 CUUCGUCUUUGCA 13
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RESULT 2
US-09-508-753B-60
; Sequence 60, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 60
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-60

Query Match 61.5%; Score 8; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 0;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Qy          5 GUCUUUGC 12
              |:|:::||
Db          2 GTCTTTGC 9
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RESULT 3
US-09-585-599A-3
; Sequence 3, Application US/09585599A
; Patent No. 6544780
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE THAT MIMICS NATURAL VIRAL INFECTION AND INDUCES LC
; TITLE OF INVENTION: LASTING IMMUNITY TO PATHOGENS
; FILE REFERENCE: 22488-706
; CURRENT APPLICATION NUMBER: US/09/585,599A
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:

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;   OTHER INFORMATION: Modified RNA editing site.
US-09-585-599A-3

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  Best Local Similarity   87.5%;  Pred. No. 0;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUU 9
              ||| ||||
Db          1 UUCUUCUU 8


RESULT 4
US-09-585-599A-5/c
; Sequence 5, Application US/09585599A
; Patent No. 6544780
; GENERAL INFORMATION:
;  APPLICANT: Wang, Danher
;  TITLE OF INVENTION: GENETIC VACCINE THAT MIMICS NATURAL VIRAL INFECTION AND INDUCES L
;  TITLE OF INVENTION:  LASTING IMMUNITY TO PATHOGENS
;  FILE REFERENCE: 22488-706
;  CURRENT APPLICATION NUMBER: US/09/585,599A
;  CURRENT FILING DATE:  2000-06-02
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: DNA of modified RNA editing site.
US-09-585-599A-5

  Query Match             49.2%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   25.0%;  Pred. No. 0;
  Matches    2;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUU 9
              ::| :|::
Db          8 TTCTTCTT 1


RESULT 5
US-09-514-245-45
; Sequence 45, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
;  APPLICANT:  JESTIN, Andre
;  APPLICANT:  ALBINA, Emanuel
;  APPLICANT:  Le CANN, Pierre
;  APPLICANT:  BLANCHARD, Phillipe
;  APPLICANT:  HUTET, Evelyne
;  APPLICANT:  ARNAULD, Claire
;  APPLICANT:  TRUONG, Catherine
;  APPLICANT:  MAHE, Dominique
;  APPLICANT:  CARIOLET, Roland
;  APPLICANT:  MADEC, Francois
;  TITLE OF INVENTION:  CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
;  FILE REFERENCE:  065691/0176
;  CURRENT APPLICATION NUMBER: US/09/514,245
;  CURRENT FILING DATE:  2000-02-28
;  PRIOR APPLICATION NUMBER:  FR 97/15396
;  PRIOR FILING DATE:  1997-12-05
;  NUMBER OF SEQ ID NOS:  170
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 45
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Type A PWD circovirus
US-09-514-245-45

  Query Match             49.2%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   37.5%;  Pred. No. 0;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUU 9
              : ||:|::
Db          1 TCCGTCTT 8


RESULT 6
US-10-327-294-3
; Sequence 3, Application US/10327294
; Patent No. 6964762
; GENERAL INFORMATION:
;  APPLICANT: Wang, Danher
;  TITLE OF INVENTION: COMPOSITION AND METHOD FOR STIMULATING IMMUNE RESPONSE TO PATHOGEN
;  TITLE OF INVENTION:  COMPLEX ADENOVIRAL VECTOR
;  FILE REFERENCE: 22488-748
;  CURRENT APPLICATION NUMBER: US/10/327,294
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: 09/585,599
;  PRIOR FILING DATE: 2000-06-02
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 8
;   TYPE: RNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Modified RNA editing site
US-10-327-294-3

  Query Match             49.2%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 0;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUU 9
              ||| ||||
Db          1 UUCUUCUU 8


RESULT 7
US-10-327-294-5/c
; Sequence 5, Application US/10327294
; Patent No. 6964762
; GENERAL INFORMATION:
;  APPLICANT: Wang, Danher
;  TITLE OF INVENTION: COMPOSITION AND METHOD FOR STIMULATING IMMUNE RESPONSE TO PATHOGEN
;  TITLE OF INVENTION:  COMPLEX ADENOVIRAL VECTOR
;  FILE REFERENCE: 22488-748
;  CURRENT APPLICATION NUMBER: US/10/327,294
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: 09/585,599
;  PRIOR FILING DATE: 2000-06-02
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: DNA of modified RNA editing site
US-10-327-294-5

  Query Match             49.2%;  Score 6.4;  DB 1;  Length 8;
  Best Local Similarity   25.0%;  Pred. No. 0;
  Matches    2;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 UUCGUCUU 9
              ::| :|::
Db          8 TTCTTCTT 1


RESULT 8
US-09-432-020B-43/c
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; Sequence 43, Application US/09432020B
; Patent No. 6268147
; GENERAL INFORMATION:
; APPLICANT: Maldonado Rodriquez, Rogelio
; APPLICANT: Beattie, Kenneth Loren
; TITLE OF INVENTION: Nucleic Acid Analysis Using Sequence-Targeted
; TITLE OF INVENTION: Tandem Hybridization
; FILE REFERENCE: D6183
; CURRENT APPLICATION NUMBER: US/09/432,020B
; CURRENT FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/106,655
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 55
; SEQ ID NO 43
; LENGTH: 7
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: CF198 probe; the 3'terminal cytidine contains
; OTHER INFORMATION: an aminopropanol which covalently binds to
; OTHER INFORMATION: the epoxysilanized glass
US-09-432-020B-43

Query Match 46.2%; Score 6; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 0;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGUCUU 9
||:|::
Db 6 CGTCTT 1

Search completed: September 1, 2006, 12:05:44
Job time : 0.001 secs